

OIEP

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/825,882

DATE: 11/30/2001
 TIME: 12:05:39

Input Set : A:\279152rx.app
 Output Set: N:\CRF3\11212001\I825882.raw

ENTERED

3 <110> APPLICANT: ADLER, JON ELLIOT
 5 <120> TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
 7 <130> FILE REFERENCE: 078003/0279152/RXT
 9 <140> CURRENT APPLICATION NUMBER: 09/825,882
 10 <141> CURRENT FILING DATE: 2001-04-05
 12 <150> PRIOR APPLICATION NUMBER: 60/195,532
 13 <151> PRIOR FILING DATE: 2000-04-07
 15 <150> PRIOR APPLICATION NUMBER: 60/247,014
 16 <151> PRIOR FILING DATE: 2000-11-13
 18 <160> NUMBER OF SEQ ID NOS: 31
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1002
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <400> SEQUENCE: 1
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 29 atttcagtc tggagtttgc agtgggggtt ctgaccaatg ccttcgtttt cttggtgaat 120
 30 ttttgggatg tagtgaagag gcaggcactg agcaacagt attgtgtgct gctgtgtctc 180
 31 agcatcagcc ggcttttccct gcattggactg ctgttccctga gtgctatcca gcttaccac 240
 32 ttcagaagt tgagtgaacc actgaaccac agctaccaag ccatcatcat gctatggatg 300
 33 attgcaaac aagccaacct ctggcttgct gctgacctca gctgcttta ctgctccaag 360
 34 ctcatccgtt tctctcacac ctctctgac tgcttgcaa gctgggtctc caggaagatc 420
 35 tcccagatgc tctgggtat tattctttgc tctgcatct gcactgtcct ctgtgtttgg 480
 36 tgctttttta gcagacctca ctccacagtc acaactgtgc tattcatgaa taacaataca 540
 37 aggtcgaact ggcagattaa agatctcaat ttattttatt cctttctctt ctgctatctg 600
 38 tggctctgtc ctcttttccct attgtttctg gtttctctg ggatgctgac tgtctccctg 660
 39 ggaaggcaca tgaggacaat gaagggtctat accagaaact ctctgaccc cagcctggag 720
 40 gccacatta aagccctcaa gtctcttgct tcttttttct gcttctttgt gatatcatcc 780
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 42 gtttgtgttg ggataatggc agcttgctcc tctgggcatg cagccatcct gatctcaggc 900
 43 aatgccaaagt tgaggagagc tgtgatgacc attctgctct gggctcagag cagcctgaag 960
 44 gtaagagccg accacaaggc agattcccgg aactgtgct ga 1002
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 48 <211> LENGTH: 333
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 50 <213> ORGANISM: Homo sapiens
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 56 Thr Phe Leu Phe Ile Ser Val Leu Glu Phe Ala Val Gly Phe Leu Thr
 57 20 25 30
 59 Asn Ala Phe Val Phe Leu Val Asn Phe Trp Asp Val Val Lys Arg Gln
 60 35 40 45
 62 Ala Leu Ser Asn Ser Asp Cys Val Leu Leu Cys Leu Ser Ile Ser Arg
 63 50 55 60
 65 Leu Phe Leu His Gly Leu Leu Phe Leu Ser Ala Ile Gln Leu Thr His

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66 65          70          75          80
68 Phe Gln Lys Leu Ser Glu Pro Leu Asn His Ser Tyr Gln Ala Ile Ile
69          85          90          95
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72          100          105          110
74 Leu Ser Leu Leu Tyr Cys Ser Lys Leu Ile Arg Phe Ser His Thr Phe
75          115          120          125
77 Leu Ile Cys Leu Ala Ser Trp Val Ser Arg Lys Ile Ser Gln Met Leu
78          130          135          140
80 Leu Gly Ile Ile Leu Cys Ser Cys Ile Cys Thr Val Leu Cys Val Trp
81 145          150          155          160
83 Cys Phe Phe Ser Arg Pro His Phe Thr Val Thr Thr Val Leu Phe Met
84          165          170          175
86 Asn Asn Asn Thr Arg Leu Asn Trp Gln Ile Lys Asp Leu Asn Leu Phe
87          180          185          190
89 Tyr Ser Phe Leu Phe Cys Tyr Leu Trp Ser Val Pro Pro Phe Leu Leu
90          195          200          205
92 Phe Leu Val Ser Ser Gly Met Leu Thr Val Ser Leu Gly Arg His Met
93          210          215          220
95 Arg Thr Met Lys Val Tyr Thr Arg Asn Ser Arg Asp Pro Ser Leu Glu
96 225          230          235          240
98 Ala His Ile Lys Ala Leu Lys Ser Leu Val Ser Phe Phe Cys Phe Phe
99          245          250          255
101 Val Ile Ser Ser Cys Val Ala Phe Ile Ser Val Pro Leu Leu Ile Leu
102          260          265          270
104 Trp Arg Asp Lys Ile Gly Val Met Val Cys Val Gly Ile Met Ala Ala
105          275          280          285
107 Cys Pro Ser Gly His Ala Ala Ile Leu Ile Ser Gly Asn Ala Lys Leu
108          290          295          300
110 Arg Arg Ala Val Met Thr Ile Leu Leu Trp Ala Gln Ser Ser Leu Lys
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114          325          330
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125 atacatgcag ctgaatgggt tcaaaataag gcagtttcca caagtggcag gatcctggtt 180
126 ttcttgagtg tatccagaat agctctccaa agcctcatga tgttagaaat taccatcagc 240
127 tcaacctccc taagttttta ttctgaagac gctgtatatt atgcattcaa aataagtttt 300
128 atattcttaa atttttgtag cctgtggttt gctgcctggc tcagttttct ctactttgtg 360
129 aagattgcc aattctccta ccccttttct ctcaaactga ggtggagaat tactggattg 420
130 ataccttggc ttctgtggct gtccgtgttt atttcttcca gtcacagcat gttctgcata 480
131 aacatctgca ctgtgtattg taacaattct ttccctatcc actcctccaa ctccactaag 540
132 aaaacatact tgtctgagat caatgtggtc ggtctggctt tttcttttaa cctggggatt 600
133 gtgactcctc tgatcatggt catcctgaca gccaccctgc tgatcctctc tctcaagaga 660

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134 cacaccctac acatgggaag caatgccaca gggccaacg accccagcat ggaggctcac 720
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136 ctgtttatct acctgtccaa catgtttgac atcaacagtc tgtggaataa tttgtgccag 840
137 atcatcatgg ctgectaccc tgccagccac tcaattctac tgattcaaga taaccctggg 900
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139 ctgtga 966
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143 <211> LENGTH: 321
144 <212> TYPE: PRT
145 <213> ORGANISM: Homo sapiens
147 <400> SEQUENCE: 4
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151 Ile Thr Leu Ile Leu Ala Val Leu Leu Ala Glu Tyr Leu Ile Gly Ile
152 20 25 30
154 Ile Ala Asn Gly Phe Ile Met Ala Ile His Ala Ala Glu Trp Val Gln
155 35 40 45
157 Asn Lys Ala Val Ser Thr Ser Gly Arg Ile Leu Val Phe Leu Ser Val
158 50 55 60
160 Ser Arg Ile Ala Leu Gln Ser Leu Met Met Leu Glu Ile Thr Ile Ser
161 65 70 75 80
163 Ser Thr Ser Leu Ser Phe Tyr Ser Glu Asp Ala Val Tyr Tyr Ala Phe
164 85 90 95
166 Lys Ile Ser Phe Ile Phe Leu Asn Phe Cys Ser Leu Trp Phe Ala Ala
167 100 105 110
169 Trp Leu Ser Phe Phe Tyr Phe Val Lys Ile Ala Asn Phe Ser Tyr Pro
170 115 120 125
172 Leu Phe Leu Lys Leu Arg Trp Arg Ile Thr Gly Leu Ile Pro Trp Leu
173 130 135 140
175 Leu Trp Leu Ser Val Phe Ile Ser Phe Ser His Ser Met Phe Cys Ile
176 145 150 155 160
178 Asn Ile Cys Thr Val Tyr Cys Asn Asn Ser Phe Pro Ile His Ser Ser
179 165 170 175
181 Asn Ser Thr Lys Lys Thr Tyr Leu Ser Glu Ile Asn Val Val Gly Leu
182 180 185 190
184 Ala Phe Phe Phe Asn Leu Gly Ile Val Thr Pro Leu Ile Met Phe Ile
185 195 200 205
187 Leu Thr Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr Leu His
188 210 215 220
190 Met Gly Ser Asn Ala Thr Gly Ser Asn Asp Pro Ser Met Glu Ala His
191 225 230 235 240
193 Met Gly Ala Ile Lys Ala Ile Ser Tyr Phe Leu Ile Leu Tyr Ile Phe
194 245 250 255
196 Asn Ala Val Ala Leu Phe Ile Tyr Leu Ser Asn Met Phe Asp Ile Asn
197 260 265 270
199 Ser Leu Trp Asn Asn Leu Cys Gln Ile Ile Met Ala Ala Tyr Pro Ala
200 275 280 285
202 Ser His Ser Ile Leu Leu Ile Gln Asp Asn Pro Gly Leu Arg Arg Ala
203 290 295 300

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214 <212> TYPE: DNA
215 <213> ORGANISM: Homo sapiens
217 <400> SEQUENCE: 5
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220 gccatctatg gggctgagtg ggccaggggc aaaacactcc ccactgggta ccgcattatg 180
221 ttgatgctga gcttttccag gctcttgcta cagatttgga tgatgctgga gaacattttc 240
222 agtctgctat tccgaattgt ttataaccaa aactcagtgat atatcctctt caaagtcata 300
223 actgtctttc tgaaccattc caatctctgg ttgctgcctt ggctcaaagt cttctattgt 360
224 cttagaattg caaacttcaa tcataccttg ttcttctga tgaagaggaa aatcatagt 420
225 ctgatgcctt ggccttctcag gctgtcagtg ttggtttctt taagcttcag ctttctcttc 480
226 tcgagagatg tcttcaatgt gtatgtgaat agctccattc ctatcccttc ctccaactcc 540
227 acggagaaga agtacttctc tgagaccaat atggteaacc tggatttttt ctataacatg 600
228 gggatcttcg ttctctgat catgttcata ctggcagcca cctgctgat cctctctctc 660
229 aagagacaca ccctacacat gggaagcaat gccacagggg ccagggaccc cagcatgaag 720
230 gctcacatag gggccatcaa agccaccagc tacttttctc tctctacat tttcaatgca 780
231 attgctctat ttctttccac gtccaacata ttgacactt acagtctctg gaatattttg 840
232 tqcaagatca tcatggctgc ctaccctgcc ggccactcag tacaactgat cttgggcaac 900
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239 <212> TYPE: PRT
240 <213> ORGANISM: Homo sapiens
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246 Lys Val Thr Phe Thr Leu Val Val Ser Gly Ile Glu Cys Ile Thr Gly
247 20 25 30
249 Ile Leu Gly Ser Gly Phe Ile Thr Ala Ile Tyr Gly Ala Glu Trp Ala
250 35 40 45
252 Arg Gly Lys Thr Leu Pro Thr Gly Asp Arg Ile Met Leu Met Leu Ser
253 50 55 60
255 Phe Ser Arg Leu Leu Leu Gln Ile Trp Met Met Leu Glu Asn Ile Phe
256 65 70 75 80
258 Ser Leu Leu Phe Arg Ile Val Tyr Asn Gln Asn Ser Val Tyr Ile Leu
259 85 90 95
261 Phe Lys Val Ile Thr Val Phe Leu Asn His Ser Asn Leu Trp Phe Ala
262 100 105 110
264 Ala Trp Leu Lys Val Phe Tyr Cys Leu Arg Ile Ala Asn Phe Asn His
265 115 120 125
267 Pro Leu Phe Phe Leu Met Lys Arg Lys Ile Ile Val Leu Met Pro Trp
268 130 135 140
270 Leu Leu Arg Leu Ser Val Leu Val Ser Leu Ser Phe Ser Phe Pro Leu

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271 145          150          155          160
273 Ser Arg Asp Val Phe Asn Val Tyr Val Asn Ser Ser Ile Pro Ile Pro
274          165          170          175
276 Ser Ser Asn Ser Thr Glu Lys Lys Tyr Phe Ser Glu Thr Asn Met Val
277          180          185          190
279 Asn Leu Val Phe Phe Tyr Asn Met Gly Ile Phe Val Pro Leu Ile Met
280          195          200          205
282 Phe Ile Leu Ala Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr
283          210          215          220
285 Leu His Met Gly Ser Asn Ala Thr Gly Ser Arg Asp Pro Ser Met Lys
286 225          230          235          240
288 Ala His Ile Gly Ala Ile Lys Ala Thr Ser Tyr Phe Leu Ile Leu Tyr
289          245          250          255
291 Ile Phe Asn Ala Ile Ala Leu Phe Leu Ser Thr Ser Asn Ile Phe Asp
292          260          265          270
294 Thr Tyr Ser Ser Trp Asn Ile Leu Cys Lys Ile Ile Met Ala Ala Tyr
295          275          280          285
297 Pro Ala Gly His Ser Val Gln Leu Ile Leu Gly Asn Pro Gly Leu Arg
298          290          295          300
300 Arg Ala Trp Lys Arg Phe Gln His Gln Val Pro Leu Tyr Leu Lys Gly
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315 atctcctttg ctgaccaaatt tctcactgct ctggcggtct ccagagttgg ttgctctg 180
316 gtattattat taaactggta ttcaactgtg ttgaatccag cttttaatag tgtagaagta 240
317 agaactactg cttataatat ctgggcagtg atcaaccatt tcagcaactg gcttgctact 300
318 accctcagca tattttatatt gctcaagatt gccaatctct ccaactttat tttctttcac 360
319 ttaaagagga gagttaagag tgtcattctg gtgatgttgt tggggccttt gctatttttg 420
320 gcttgctatc tttttgtgat aaacatgaat gagattgtgc ggacaaaaga atttgaagga 480
321 aacatgactt ggaagatcaa attgaagagt gcaatgtact tttcaaatat gactgtaacc 540
322 atggtagcaa acttagtacc cttcactctg accctactat cttttatgct gttaatctgt 600
323 tctttgtgta aacatctcaa gaagatgcag ctccatggtg aaggatctca agatcccagc 660
324 accaaggtcc acataaaagc ttgcaaact gtgatctcct tctcttggtt atgtgccatt 720
325 tactttctgt ccataatgat atcagtttgg agttttggaa gtctggaaaa caaacctgtc 780
326 ttcattgtct gcaaagctat tagattcagc tctccttcaa tccaccatt catcctgatt 840
327 tggggaacaa agaagctaaa gcagactttt ctttcagttt tttggcaaat gaggtactgg 900
328 gtgaaaggag agaagacttc atctccatag          930
331 <210> SEQ ID NO: 8
332 <211> LENGTH: 309
333 <212> TYPE: PRT
334 <213> ORGANISM: Homo sapiens
336 <400> SEQUENCE: 8
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Use of n and / or Xaa has been detected in this Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/825,882

DATE: 11/30/2001

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Input Set : A:\279152rx.app

Output Set: N:\CRF3\11212001\I825882.raw

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L:1124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30